

# SEQUENCE LISTING

<110> Mack, David  
Gish, Kurt  
Wilson, Keith

<120> NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR CANCER MODULATORS

<130> A-69192-1/DJB/JJD/AMS

<150> US 09/608,821

<151> 2000-06-30

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<170> PatentIn version 3.0

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Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile	
425 430 435	
gtg att ttt tac tac ctg ggc tta ctg tgt ggc gtg tgc ggc tat gac	1399
Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp	
440 445 450	
agg cat gcc acc ccg acc acc cga ggc tgt gtc tcc aac acc gga ggc	1447
Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly	
455 460 465 470	
gtc ttc ctc atg gtt gga gtt gga tta agt ttc ctc ttt tgc tgg ata	1495
Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile	
475 480 485	
ttg atg atc att gtg gtt ctt acc ttt gtc ttt ggt gca aat gtg gaa	1543
Leu Met Ile Ile Val Val Leu Thr Phe Val Phe Gly Ala Asn Val Glu	
490 495 500	
aaa ctg atc tgt gaa cct tac acg agc aag gaa tta ttc cgg gtt ttg	1591
Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu	
505 510 515	
gat aca ccc tac tta cta aat gaa gac tgg gaa tac tat ctc tct ggg	1639
Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly	
520 525 530	
aag cta ttt aat aaa tca aaa atg aag ctc act ttt gaa caa gtt tac	1687
Lys Leu Phe Asn Lys Ser Lys Met Lys Leu Thr Phe Glu Gln Val Tyr	
535 540 545 550	
agt gac tgc aaa aaa aat aga ggc act tac ggc act ctt cac ctg cag	1735
Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr Gly Thr Leu His Leu Gln	
555 560 565	
aac agc ttc aat atc agt gaa cat ctc aac att aat gag cat act gga	1783

Asn	Ser	Phe	Asn	Ile	Ser	Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly		
			570					575					580				
agc	ata	agc	agt	gaa	ttg	gaa	agt	ctg	aag	gta	aat	ctt	aat	atc	ttt	1831	
Ser	Ile	Ser	Ser	Glu	Leu	Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe		
		585					590				595						
ctg	ttg	ggg	gca	gca	gga	aga	aaa	aac	ctt	cag	gat	ttt	gct	gct	tgt	1879	
Leu	Leu	Gly	Ala	Ala	Gly	Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys		
	600					605				610							
gga	ata	gac	aga	atg	aat	tat	gac	agc	tac	ttg	gct	cag	act	ggg	aaa	1927	
Gly	Ile	Asp	Arg	Met	Asn	Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys		
615					620					625					630		
tcc	ccc	gca	gga	gtg	aat	ctt	tta	tca	ttt	gca	tat	gat	cta	gaa	gca	1975	
Ser	Pro	Ala	Gly	Val	Asn	Leu	Leu	Ser	Phe	Ala	Tyr	Asp	Leu	Glu	Ala		
				635					640					645			
aaa	gca	aac	agt	ttg	ccc	cca	gga	aat	ttg	agg	aac	tcc	ctg	aaa	aga	2023	
Lys	Ala	Asn	Ser	Leu	Pro	Pro	Gly	Asn	Leu	Arg	Asn	Ser	Leu	Lys	Arg		
			650					655					660				
gat	gca	caa	act	att	aaa	aca	att	cac	cag	caa	cga	gtc	ctt	cct	ata	2071	
Asp	Ala	Gln	Thr	Ile	Lys	Thr	Ile	His	Gln	Gln	Arg	Val	Leu	Pro	Ile		
		665					670					675					
gaa	caa	tca	ctg	agc	act	cta	tac	caa	agc	gtc	aag	ata	ctt	caa	cgc	2119	
Glu	Gln	Ser	Leu	Ser	Thr	Leu	Tyr	Gln	Ser	Val	Lys	Ile	Leu	Gln	Arg		
	680					685				690							
aca	ggg	aat	gga	ttg	ttg	gag	aga	gta	act	agg	att	cta	gct	tct	ctg	2167	
Thr	Gly	Asn	Gly	Leu	Leu	Glu	Arg	Val	Thr	Arg	Ile	Leu	Ala	Ser	Leu		
695					700				705						710		
gat	ttt	gct	cag	aac	ttc	atc	aca	aac	aat	act	tcc	tct	gtt	att	att	2215	
Asp	Phe	Ala	Gln	Asn	Phe	Ile	Thr	Asn	Asn	Thr	Ser	Ser	Val	Ile	Ile		
				715					720					725			
gag	gaa	act	aag	aag	tat	ggg	aga	aca	ata	ata	gga	tat	ttt	gaa	cat	2263	
Glu	Glu	Thr	Lys	Lys	Tyr	Gly	Arg	Thr	Ile	Ile	Gly	Tyr	Phe	Glu	His		
			730				735						740				
tat	ctg	cag	tgg	atc	gag	ttc	tct	atc	agt	gag	aaa	gtg	gca	tcg	tgc	2311	
Tyr	Leu	Gln	Trp	Ile	Glu	Phe	Ser	Ile	Ser	Glu	Lys	Val	Ala	Ser	Cys		
		745					750					755					
aaa	cct	gtg	gcc	acc	gct	cta	gat	act	gct	gtt	gat	gtc	ttt	ctg	tgt	2359	
Lys	Pro	Val	Ala	Thr	Ala	Leu	Asp	Thr	Ala	Val	Asp	Val	Phe	Leu	Cys		
	760					765				770							
agc	tac	att	atc	gac	ccc	ttg	aat	ttg	ttt	tgg	ttt	ggc	ata	gga	aaa	2407	
Ser	Tyr	Ile	Ile	Asp	Pro	Leu	Asn	Leu	Phe	Trp	Phe	Gly	Ile	Gly	Lys		
775					780					785					790		
gct	act	gta	ttt	tta	ctt	ccg	gct	cta	att	ttt	gcg	gta	aaa	ctg	gct	2455	
Ala	Thr	Val	Phe	Leu	Leu	Pro	Ala	Leu	Ile	Phe	Ala	Val	Lys	Leu	Ala		
				795					800					805			
aag	tac	tat	cgt	cga	atg	gat	tcg	gag	gac	gtg	tac	gat	gat	gtt	gaa	2503	
Lys	Tyr	Tyr	Arg	Arg	Met	Asp	Ser	Glu	Asp	Val	Tyr	Asp	Asp	Val	Glu		

810

815

820

act ata ccc atg aaa aat atg gaa aat ggt aat aat ggt tat cat aaa 2551  
 Thr Ile Pro Met Lys Asn Met Glu Asn Gly Asn Asn Gly Tyr His Lys  
 825 830 835

gat cat gta tat ggt att cac aat cct gtt atg aca agc cca tca caa 2599  
 Asp His Val Tyr Gly Ile His Asn Pro Val Met Thr Ser Pro Ser Gln  
 840 845 850

cat tga tagctgatgt tgaaactgct tgagcatcag gataactcaaa gtggaaagga 2655  
 His  
 855

tcacagattt ttggtagttt ctgggtctac aaggactttc caaatccagg agcaacgcca 2715

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ttaaacaat gagtattata ggactttctt ctaaatagagc taaataagtc accattgact 3135

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<210> 4

<211> 855

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Leu Val Leu Gly Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn



Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys Ser Leu His Gln  
260 265 270

Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val Lys Thr Ser Leu  
275 280 285

Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His Pro Ser Ser Glu  
290 295 300

Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro  
305 310 315 320

Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu Asp Asn Val Asn  
325 330 335

Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln  
340 345 350

Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln Thr Thr Thr Val  
355 360 365

Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly Ser Asp Ile Asp  
370 375 380

Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser  
385 390 395 400

Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg Asn Leu Pro Thr  
405 410 415

Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys  
420 425 430

Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys  
435 440 445

Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr Thr Arg Gly Cys  
450 455 460

Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly Val Gly Leu Ser  
465 470 475 480

Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val Leu Thr Phe Val  
485 490 495

Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys  
500 505 510

Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp  
515 520 525

Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser Lys Met Lys Leu  
530 535 540

Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr  
545 550 555 560

Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser Glu His Leu Asn  
565 570 575

Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys  
580 585 590

Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu  
595 600 605

Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr  
610 615 620

Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn Leu Leu Ser Phe  
625 630 635 640

Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu  
645 650 655

Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys Thr Ile His Gln  
660 665 670

Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser  
675 680 685

Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu Glu Arg Val Thr  
690 695 700

Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn  
705 710 715 720

Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile  
725 730 735



Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser  
740 745 750

Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala Leu Asp Thr Ala  
755 760 765

Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe  
770 775 780

Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu Pro Ala Leu Ile  
785 790 795 800

Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp  
805 810 815

Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn Met Glu Asn Gly  
820 825 830

Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile His Asn Pro Val  
835 840 845

Met Thr Ser Pro Ser Gln His  
850 855

<210> 5

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Extracellular cytokine receptor motif found in many species.

<220>

<221> UNSURE

<222> (3)..(3)

<223> "Xaa" at position 3 can be any amino acid.

<400> 5

Trp Ser Xaa Trp Ser  
1 5